SEQUENCE LISTING

<110> Ajinomoto Co., Inc.

<120> Method for Producing Subunit Peptide Originating from Oligomeric Protein

<130> B-586AYOP964

<150> JP 11-96073

<151> 1999-04-02

<160> 10

<210> 1

<211> 126

<212> PRT

<213> Crotalus horridus horridus

<400> 1

Asp Leu Glu Cys Pro Ser Gly Trp Ser Ser Tyr Asp Arg Tyr Cys Tyr 1 5 10 15

Lys Pro Phe Lys Gln Glu Met Thr Trp Ala Asp Ala Glu Arg Phe Cys
20 25 30

Ser Glu Gln Ala Lys Gly Gly His Leu Leu Ser Val Glu Thr Ala Leu 35 40 45

Glu Ala Ser Phe Val Asp Asn Val Leu Tyr Ala Asn Lys Glu Tyr Leu 50 55 60

Thr Arg Tyr Ile Trp Ile Gly Leu Arg Val Gln Asn Lys Gly Gln Pro 65 70 75 80

Cys Ser Ser Ile Ser Tyr Glu Asn Leu Val Asp Pro Phe Glu Cys Phe
85 90 95

Met Val Ser Arg Asp Thr Arg Leu Arg Glu Trp Phe Lys Val Asp Cys
100 105 110

Glu Gln Gln His Ser Phe Ile Cys Lys Phe Thr Arg Pro Arg 115 120 125

<210> 2

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

```
<223> Description of Artificial Sequence: primer
<220>
<221> misc_feature
<222> (12)
<223> n=a, g, c or t
<400> 2
                                                                     17
cargaratga cntgggc
<210> 3
<211> 17
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: primer
<220>
<221> misc_feature
<222> (3)
\langle 223 \rangle n=a, g, c or t
<400> 3
                                                                     17
tcnacyttra accaytc
<210> 4
<211> 272
<212> DNA
<213> Crotalus horridus horridus
<400> 4
caggagatga cttgggccga tgcagagagg ttctgctcgg agcaggcgaa gggcgggcat 60
ctcctctctg tcgaaaccgc cctagaagca tcctttgtgg acaatgtgct ctatgcgaac 120
aaagagtacc tcacacgtta tatctggatt ggactgaggg ttcaaaacaa aggacagcca 180
tgctccagca tcagttatga gaacctggtt gacccatttg aatgttttat ggtgagcaga 240
                                                                     272
gacacaagge ttegtgagtg gtteaaagte ga
<210> 5
<211> 690
<212> DNA
<213> Crotalus horridus horridus
```

<220> <221> CDS <222> (96)..(512) <400> 5 ctgagcagac ttgctacctg tggaggccga ggaacagttc tctctgcagg gaaggaaaga 60 acgcc atg ggg cga ttc atc ttc gtg agc ttc aac ttg ctg gtc gtg ttc 110 Met Gly Arg Phe Ile Phe Val Ser Phe Asn Leu Leu Val Val Phe 10 ctc tcc cta agt gga act cta gct gat ttg gaa tgt ccc tcc ggt tgg 158 Leu Ser Leu Ser Gly Thr Leu Ala Asp Leu Glu Cys Pro Ser Gly Trp 25 20 tet tee tat gat egg tat tge tae aag eec tte aaa eaa gag atg ace 206 Ser Ser Tyr Asp Arg Tyr Cys Tyr Lys Pro Phe Lys Gln Glu Met Thr 45 40 35 254 tgg gcc gat gca gag agg ttc tgc tcg gag cag gcg aag ggc ggg cat Trp Ala Asp Ala Glu Arg Phe Cys Ser Glu Gln Ala Lys Gly Gly His 50 55 302 ctc ctc tct gtc gaa acc gcc cta gaa gca tcc ttt gtg gac aat gtg Leu Leu Ser Val Glu Thr Ala Leu Glu Ala Ser Phe Val Asp Asn Val 65 ctc tat gcg aac aaa gag tac ctc aca cgt tat atc tgg att gga ctg 350 Leu Tyr Ala Asn Lys Glu Tyr Leu Thr Arg Tyr Ile Trp Ile Gly Leu 80 85 90 agg gtt caa aac aaa gga cag cca tgc tcc agc atc agt tat gag aac 398 Arg Val Gln Asn Lys Gly Gln Pro Cys Ser Ser Ile Ser Tyr Glu Asn 105 ctg gtt gac cca ttt gaa tgt ttt atg gtg agc aga gac aca agg ctt 446 Leu Val Asp Pro Phe Glu Cys Phe Met Val Ser Arg Asp Thr Arg Leu 115 120 cgt gag tgg ttt aaa gtt gac tgt gaa caa caa cat tct ttc ata tgc 494 Arg Glu Trp Phe Lys Val Asp Cys Glu Gln Gln His Ser Phe Ile Cys 135 130 542 aag ttc acg cga cca cgt taagatccgg ctgtgtgaag tctggagaag Lys Phe Thr Arg Pro Arg 145 caaggaagee ecceacetet ecceacece caeetteege aatetetget etteeceett 602

tgctcagtgg atgctctctg tagccggatc tgggttttct gctccagatg ggtcagaaga 662

690

<210> 6

<211> 139

tccaataaat tctgcctacc caaaaaaa

<212> PRT

<213> Crotalus horridus horridus

```
<400> 6
Met Gly Arg Phe Ile Phe Val Ser Phe Asn Leu Leu Val Val Phe Leu
                                      10
Ser Leu Ser Gly Thr Leu Ala Asp Leu Glu Cys Pro Ser Gly Trp Ser
             20
Ser Tyr Asp Arg Tyr Cys Tyr Lys Pro Phe Lys Gln Glu Met Thr Trp
Ala Asp Ala Glu Arg Phe Cys Ser Glu Gln Ala Lys Gly Gly His Leu
     50
Leu Ser Val Glu Thr Ala Leu Glu Ala Ser Phe Val Asp Asn Val Leu
                                          75
Tyr Ala Asn Lys Glu Tyr Leu Thr Arg Tyr Ile Trp Ile Gly Leu Arg
                 85
                                      90
Val Gln Asn Lys Gly Gln Pro Cys Ser Ser Ile Ser Tyr Glu Asn Leu
                                 105
Val Asp Pro Phe Glu Cys Phe Met Val Ser Arg Asp Thr Arg Leu Arg
                            120
                                                 125
Glu Trp Phe Lys Val Asp Cys Glu Gln Gln His Ser Phe Ile Cys Lys
    130
                        135
                                             140
Phe Thr Arg Pro Arg
145
<210> 7
<211> 30
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: primer
<400> 7
attggatcca tggatttgga atgtccctcc
<210> 8
<211> 30
<212> DNA
```

30

<220>

<213> Artificial Sequence

<223> Description of Artificial Sequence: primer

<400> 8	
aataagctta acgtggtcgc gtgaacttgc	30
<210> 9	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: primer	
<400> 9	
gatgctggag gctggctgtc ctttgt	26
<210> 10	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: primer	
<400> 10	
ggacagccag cctccagcat cagtta	26

SEQUENCE LISTING

<110> FUKUCHI, NAOYUKI KAGEYAMA, SHUNSUKE KITO, MORIKAZU KAYAHARA, TAKASHI YAMAMOTO, HIROSHI

- <120> Method for Producing Subunit Peptide Originating from Oligomeric Protein
- <130> 214595US0PCT
- <140> US 09/926,256
- <141> 2001-10-02
- <150> JP 11-96073
- <151> 1999-04-02
- <160> 10
- <170> PatentIn version 3.1
- <210> 1
- <211> 126
- <212> PRT
- <213> Crotalus horridus horridus
- <400> 1
- Asp Leu Glu Cys Pro Ser Gly Trp Ser Ser Tyr Asp Arg Tyr Cys Tyr 1 5 10 15
- Lys Pro Phe Lys Gln Glu Met Thr Trp Ala Asp Ala Gln Arg Phe Cys 20 25 30
- Ser Glu Gln Ala Lys Gly Gly His Leu Leu Ser Val Glu Thr Ala Leu 35 40 45
- Glu Ala Ser Phe Val Asp Asn Val Leu Tyr Ala Asn Lys Glu Tyr Leu 50 55 60
- Thr Arg Tyr Ile Trp Ile Gly Leu Arg Val Gln Asn Lys Gly Gln Pro 65 70 75 80
- Cys Ser Ser Ile Ser Tyr Glu Asn Leu Val Asp Pro Phe Glu Cys Phe 85 90 95
- Met Val Ser Arg Asp Thr Arg Leu Arg Glu Trp Phe Lys Val Asp Cys
 100 105 110

	<210>								
	<211>	17							
	<212>								
	<213>	ARTI	FICIAL SEQU	UENCE					
	<220>								
	<223>	SYNI	HETIC DNA						
	<220>								
	<221>	misc	: feature						
	<222>								
			g, c or t						
		·	J.						
	<400>	2							
			cntgggc					17	
	cargare	2034	01109990						
. Pi	<210>	2							
4	<211>								
	<211>								
			FICIAL SEQU	TENCE					
	(21)/	MILL	.FICIAL DIQ	SEIVEE .					
	<220>								
ij.	<223>	SYNT	HETIC DNA						
; 3									
មុខស្នាំ	<220>								
3185	<221>	misc	_feature						
122	<222>	(3).	. (3)						
14	<223>	n=a,	g, c or t						
1 40									
175	<400>	3							
			accaytc					17	
	conacy		acca _f cc						
	<210>								
	<211>								
•	<212>			1					
	<213>	Crot	alus norrio	dus horridus	5				
	<400>	4							
	caggaga	atga	cttgggccga	tgcagagagg	ttctgctcgg	agcaggcgaa	gggcgggcat	60	
_									
·	ctcctct	ctg	tcgaaaccgc	cctagaagca	tcctttgtgg	acaatgtgct	ctatgcgaac	120	
	aaagagt	acc	tcacacatta	tatctqqatt	ggactgaggg	ttcaaaacaa	aggacagcca	180	
	~~~9491	-400	Jacacycca		22~~~273		3 3 2 4 3 4 5 4 4	230	
	tgctcca	agca	tcagttatga	gaacctggtt	gacccatttg	aatgttttat	ggtgagcaga	240	
	~~~~	.~-	++	attana-at-	<b>~</b>			272	
	uacacaa	2DDr	LLCULGAGEG	gttcaaagtc	чa			4/4	

Glu Gln Gln His Ser Phe Ile Cys Lys Phe Thr Arg Pro Arg

<210> 5 <211> 690 <212> DNA <213> Crotalus horridus						
<220> <221> CDS <222> (66)(512) <223>						
<400> 5 ctgagcagac ttgctacctg tggaggccga ggaacagttc tctctgcagg gaaggaaaga						
acgcc atg ggg cga ttc atc ttc gtg agc ttc aac ttg ctg gtc gtg ttc Met Gly Arg Phe Ile Phe Val Ser Phe Asn Leu Leu Val Val Phe 1 5 10 15	110					
ctc tcc cta agt gga act cta gct gat ttg gaa tgt ccc tcc ggt tgg Leu Ser Leu Ser Gly Thr Leu Ala Asp Leu Glu Cys Pro Ser Gly Trp 20 25 30	158					
tct tcc tat gat cgg tat tgc tac aag ccc ttc aaa caa gag atg acc Ser Ser Tyr Asp Arg Tyr Cys Tyr Lys Pro Phe Lys Gln Glu Met Thr 35 40 45	206					
tgg gcc gat gca gag agg ttc tgc tcg gag cag gcg aag ggc ggg cat Trp Ala Asp Ala Glu Arg Phe Cys Ser Glu Gln Ala Lys Gly Gly His 50 55 60	254					
ctc ctc tct gtc gaa acc gcc cta gaa gca tcc ttt gtg gac aat gtg Leu Leu Ser Val Glu Thr Ala Leu Glu Ala Ser Phe Val Asp Asn Val 65 70 75	302					
ctc tat gcg aac aaa gag tac ctc aca cgt tat atc tgg att gga ctg Leu Tyr Ala Asn Lys Glu Tyr Leu Thr Arg Tyr Ile Trp Ile Gly Leu 80 85 90 95	350					
agg gtt caa aac aaa gga cag cca tgc tcc agc atc agt tat gag aac Arg Val Gln Asn Lys Gly Gln Pro Cys Ser Ser Ile Ser Tyr Glu Asn 100 105 110	398					
ctg gtt gac cca ttt gaa tgt ttt atg gtg agc aga gac aca agg ctt Leu Val Asp Pro Phe Glu Cys Phe Met Val Ser Arg Asp Thr Arg Leu 115 120 125	446					
cgt gag tgg ttt aaa gtt gac tgt gaa caa caa cat tct ttc ata tgc Arg Glu Trp Phe Lys Val Asp Cys Glu Gln Gln His Ser Phe Ile Cys 130 135 140	494					
aag ttc acg cga cca cgt taagatccgg ctgtgtgaag tctggagaag Lys Phe Thr Arg Pro Arg 145	542					
caaggaagee ecceacetet ecceacecee cacetteege aatetetget ettececett						
tgctcagtgg atgctctctg tagccggatc tgggttttct gctccagatg ggtcagaaga	662					

```
<210> 6
```

<211> 149

<212> PRT

<213> Crotalus horridus horridus

<400> 6

Met Gly Arg Phe Ile Phe Val Ser Phe Asn Leu Leu Val Val Phe Leu 1 5 10 15

Ser Leu Ser Gly Thr Leu Ala Asp Leu Glu Cys Pro Ser Gly Trp Ser 20 25 30

Ser Tyr Asp Arg Tyr Cys Tyr Lys Pro Phe Lys Gln Glu Met Thr Trp 35 40 45

Ala Asp Ala Glu Arg Phe Cys Ser Glu Gln Ala Lys Gly Gly His Leu 50 55 60

Leu Ser Val Glu Thr Ala Leu Glu Ala Ser Phe Val Asp Asn Val Leu 65 70 75 80

Tyr Ala Asn Lys Glu Tyr Leu Thr Arg Tyr Ile Trp Ile Gly Leu Arg 85 90 95

Val Gln Asn Lys Gly Gln Pro Cys Ser Ser Ile Ser Tyr Glu Asn Leu 100 105 110

Val Asp Pro Phe Glu Cys Phe Met Val Ser Arg Asp Thr Arg Leu Arg 115 120 125

Glu Trp Phe Lys Val Asp Cys Glu Gln Gln His Ser Phe Ile Cys Lys 130 135 140

Phe Thr Arg Pro Arg 145

<210> 7

<211> 30

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

	<223>	SYNTHETIC DNA	
	<400>	7	
		teca tggatttgga atgteeetee	30
	<210>	8	
		30	
	<212>		
	<213>	ARTIFICIAL SEQUENCE	
	<220>		
	<223>	SYNTHETIC DNA	
	<400>	8	
	aataag	ctta acgtggtcgc gtgaacttgc	30
	<210>	9	
	<211>		
140	<212>		
	<213>	ARTIFICIAL SEQUENCE	
Į	000		
	<220> <223>	SYNTHETIC DNA	
[新 昭]	\223 /	SININGIE DNA	
(a)	<400>	9	
Traff Traff (1925) Traff (1925) W.	gatgct	ggag getggetgte etttgt	26
3			
द ्यों ।	<210>	10	
	<211>	26	
	<212>	DNA	
	<213>	ARTIFICIAL SEQUENCE	
:#! :#!	<220>		
नर्मी।	<223>	SYNTHETIC DNA	
	<400>	10	
		ccag cctccagcat cagtta	26
-			